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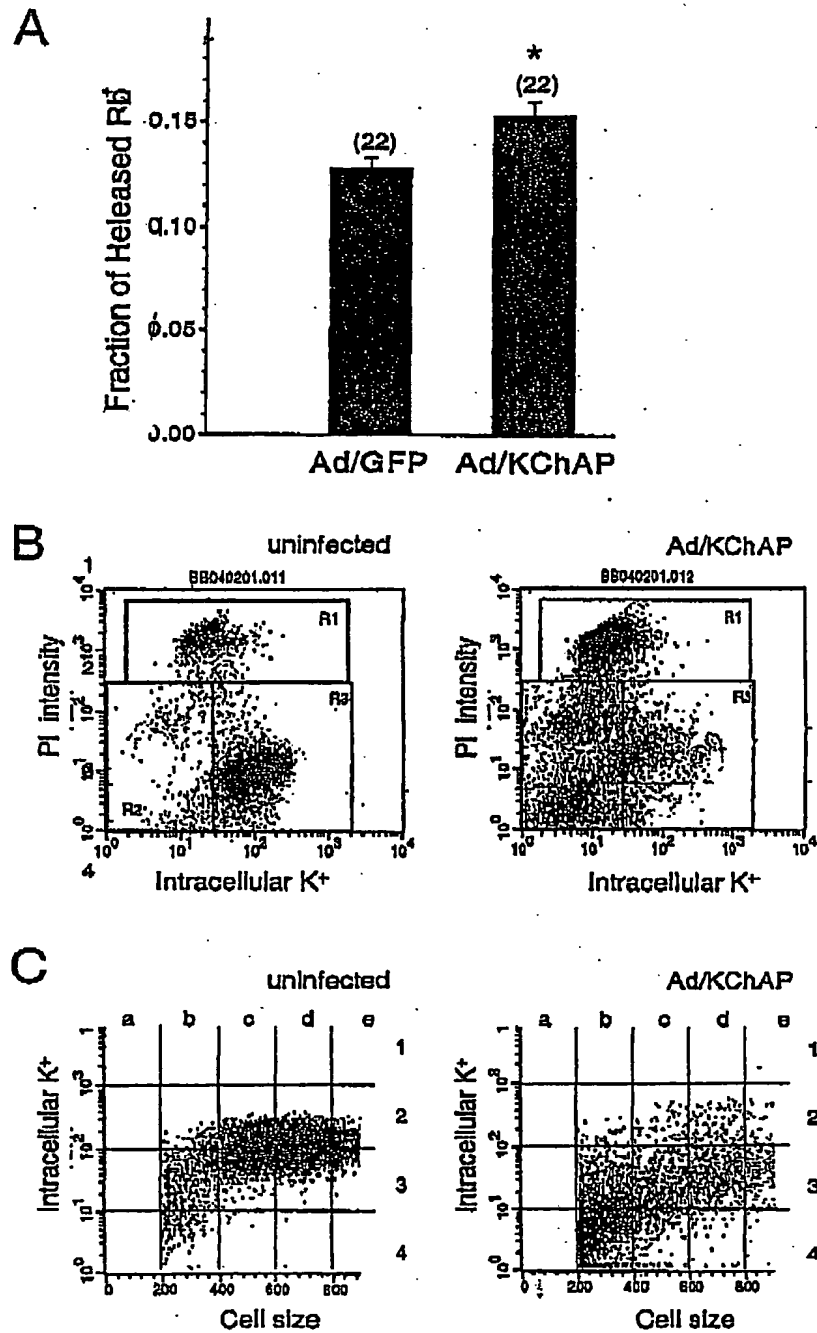


Fig. 1

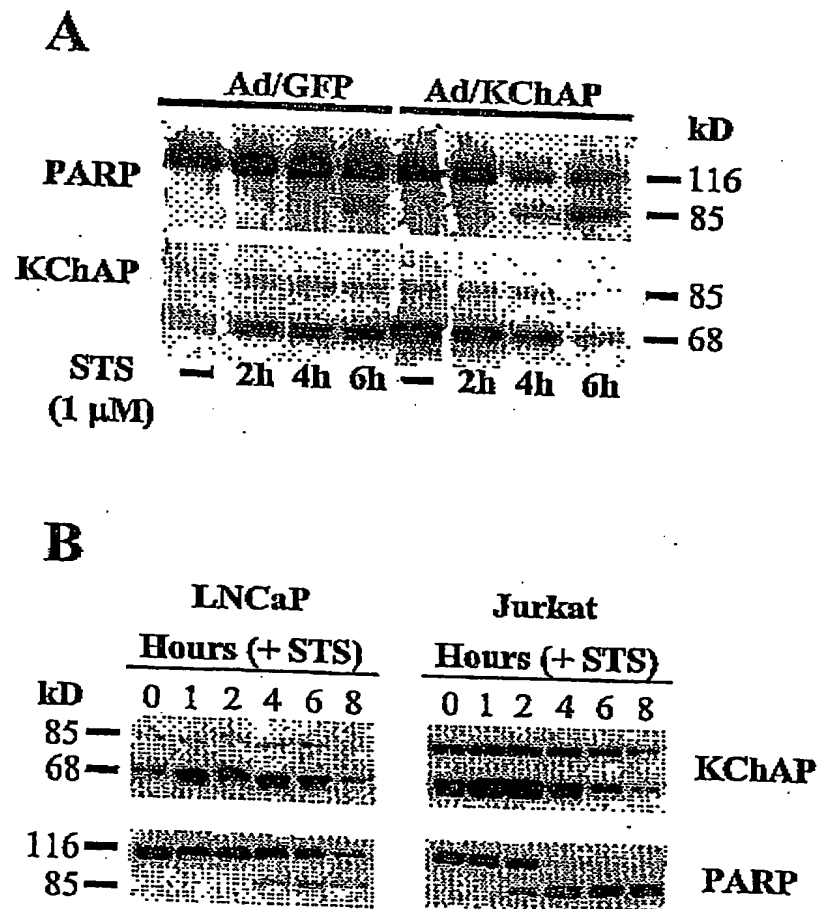


Fig. 2

Fig. 3

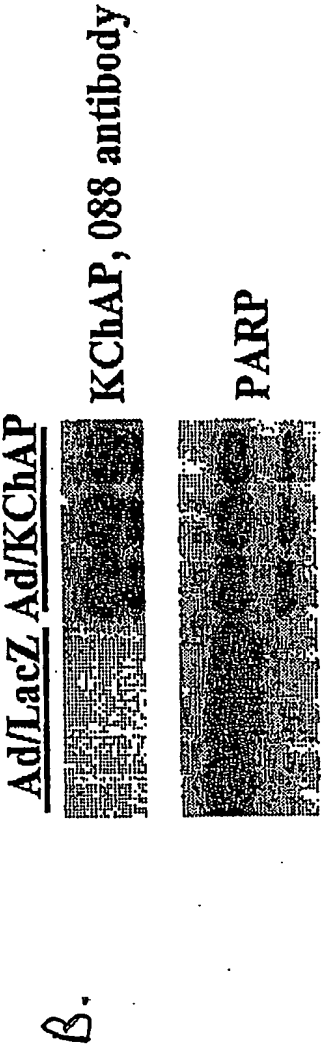
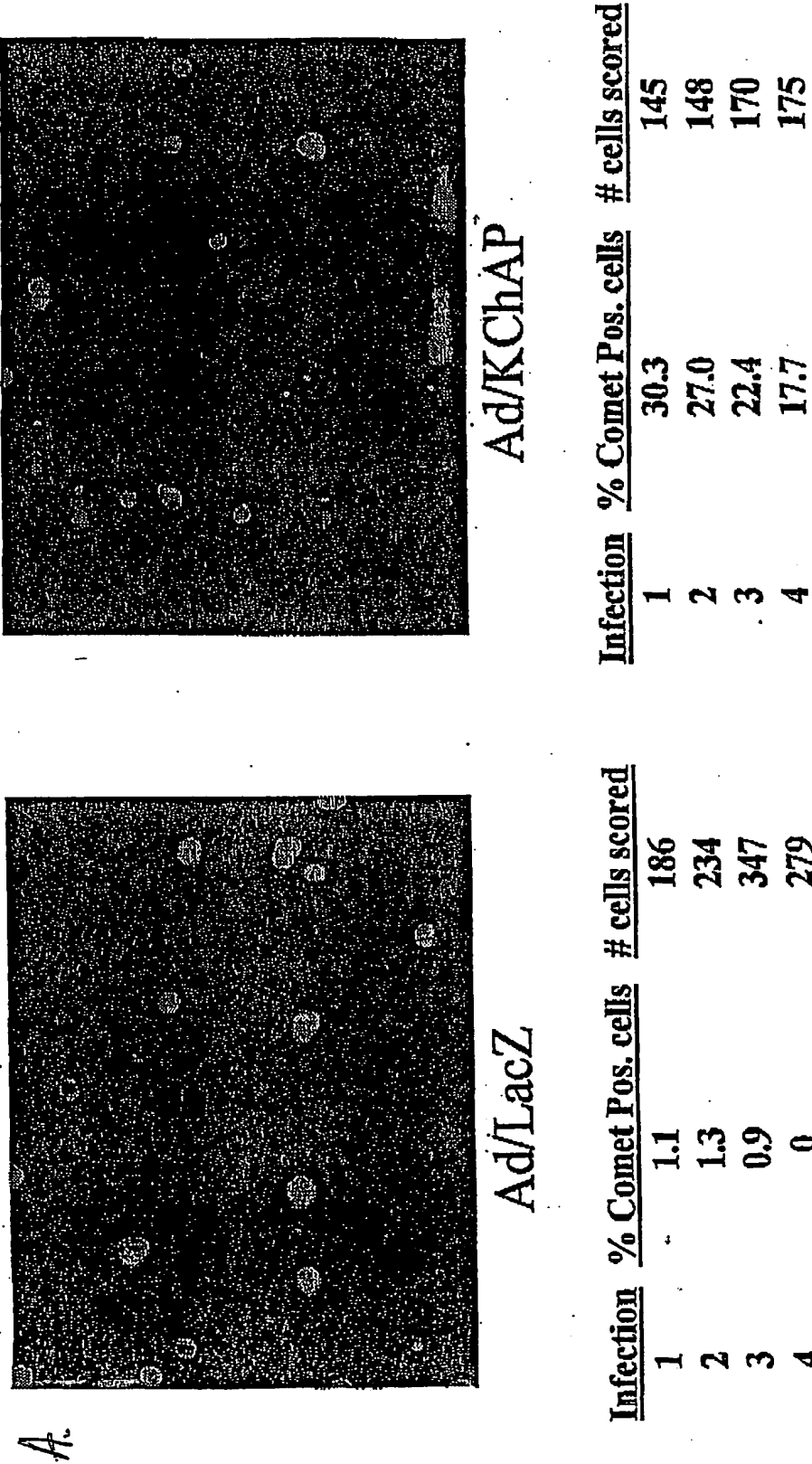


Fig. 4

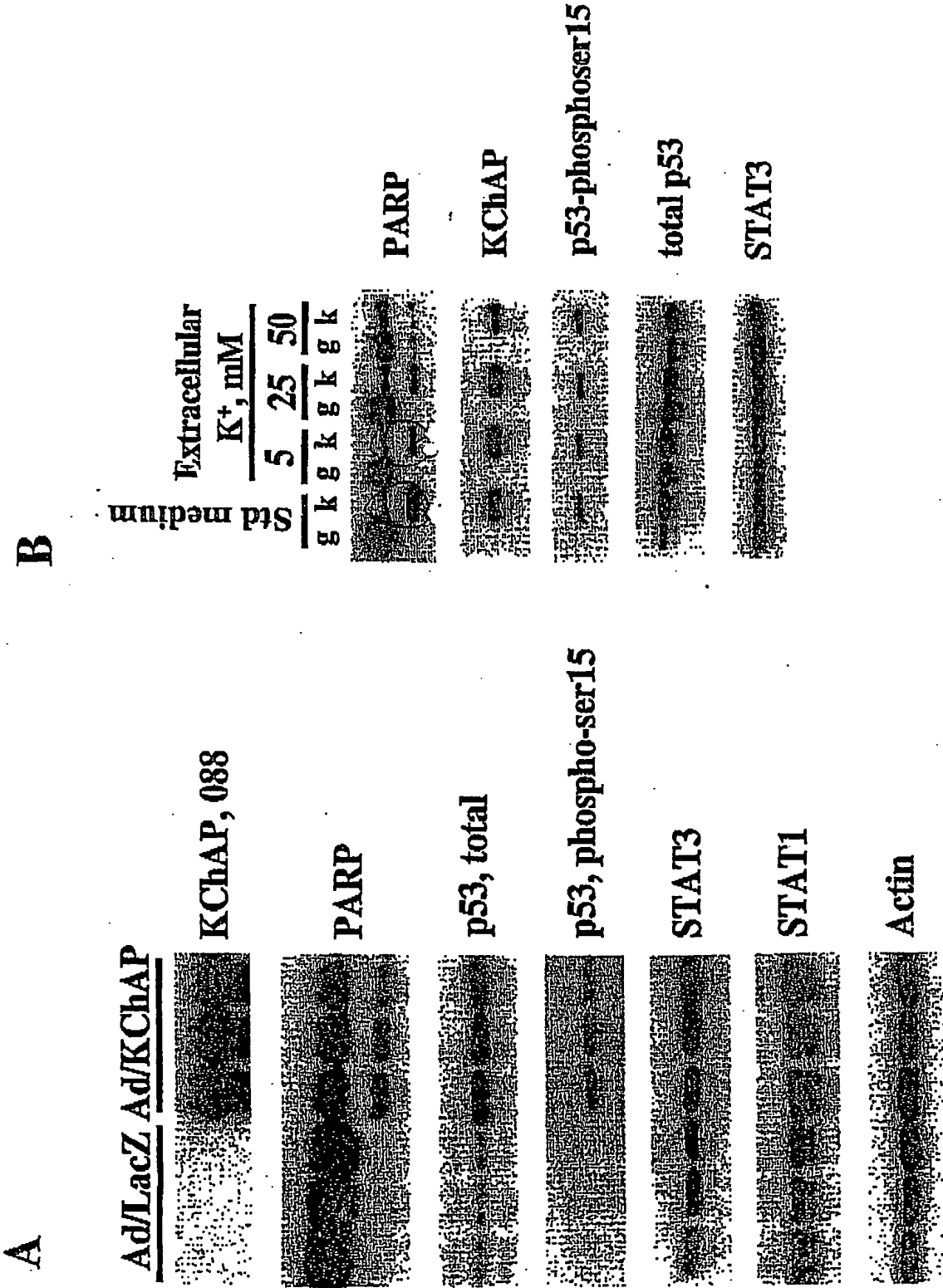


Fig. 5

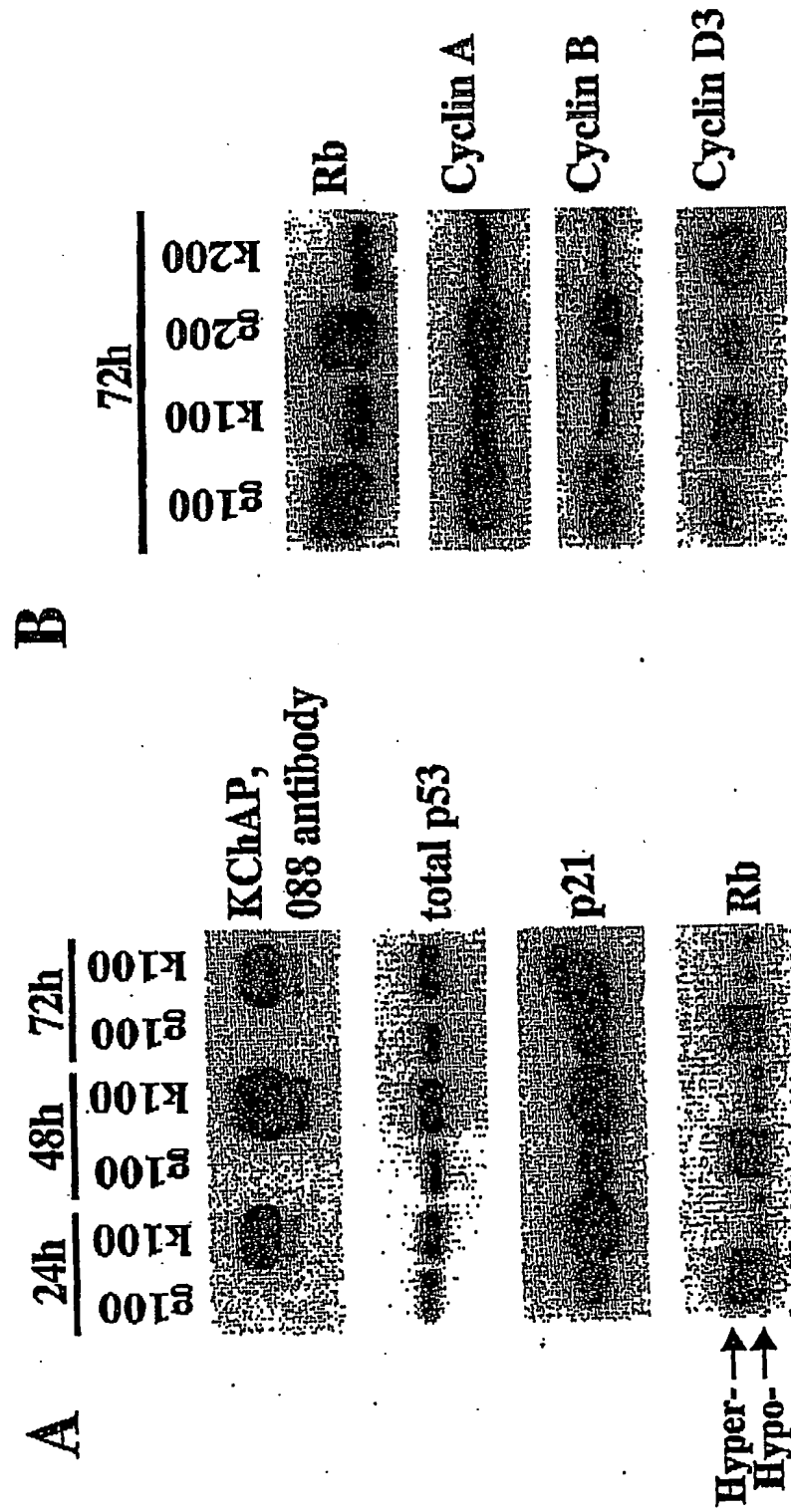
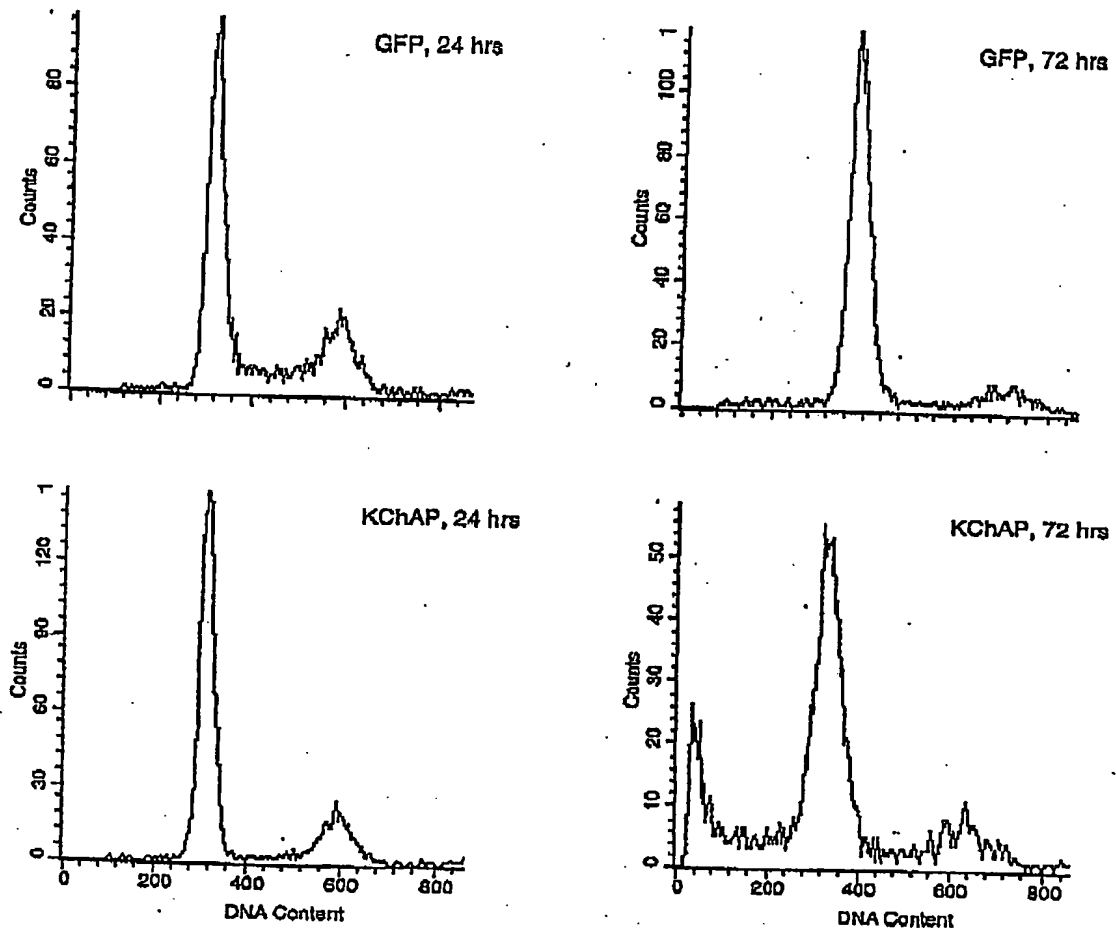


Fig. 6

A



B

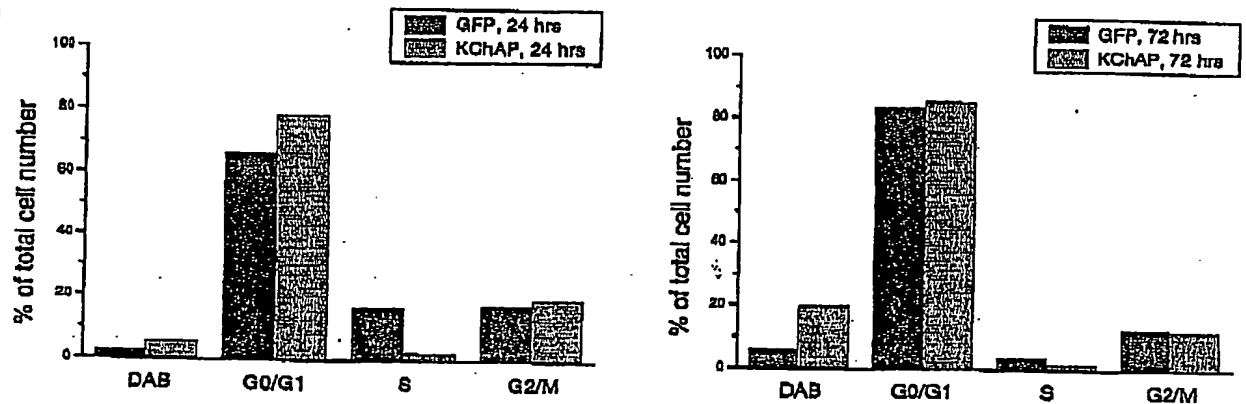


Fig. 7

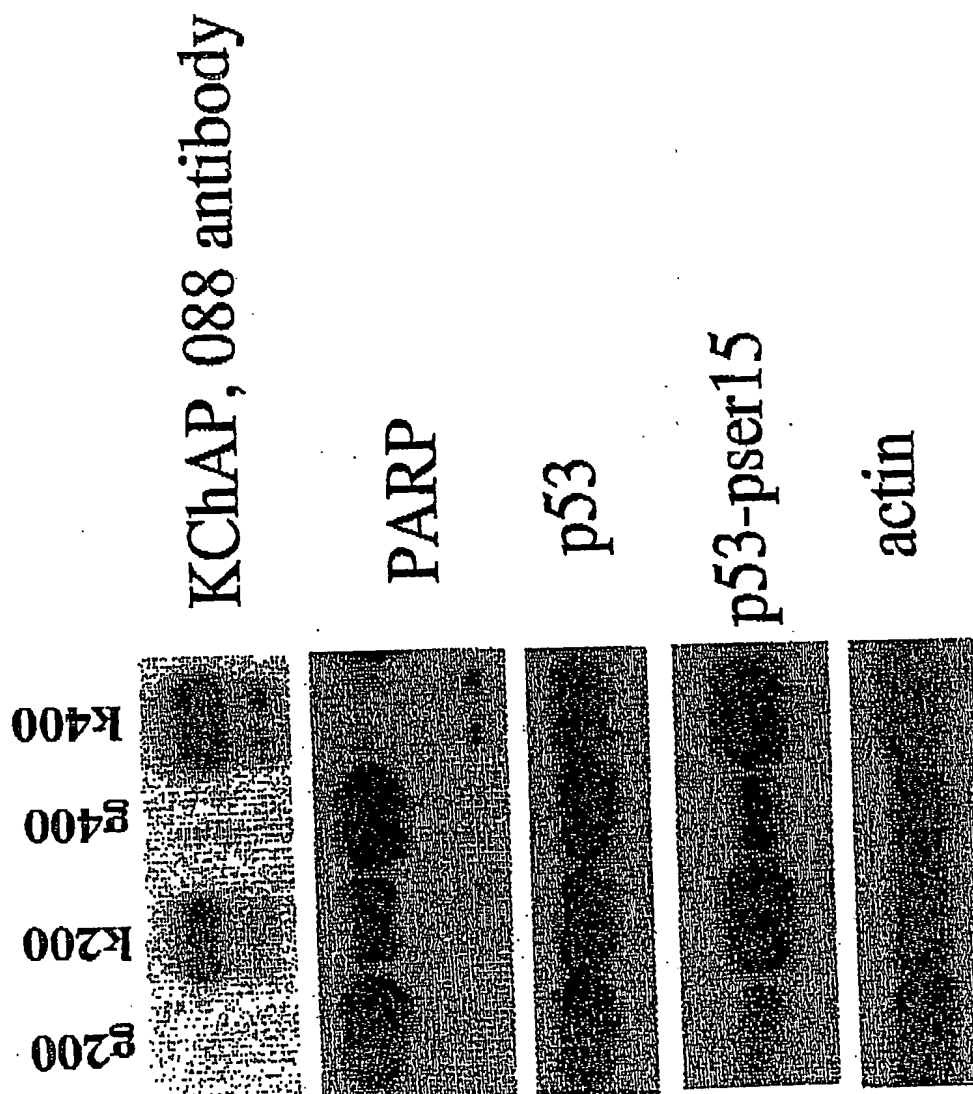




Fig. 8

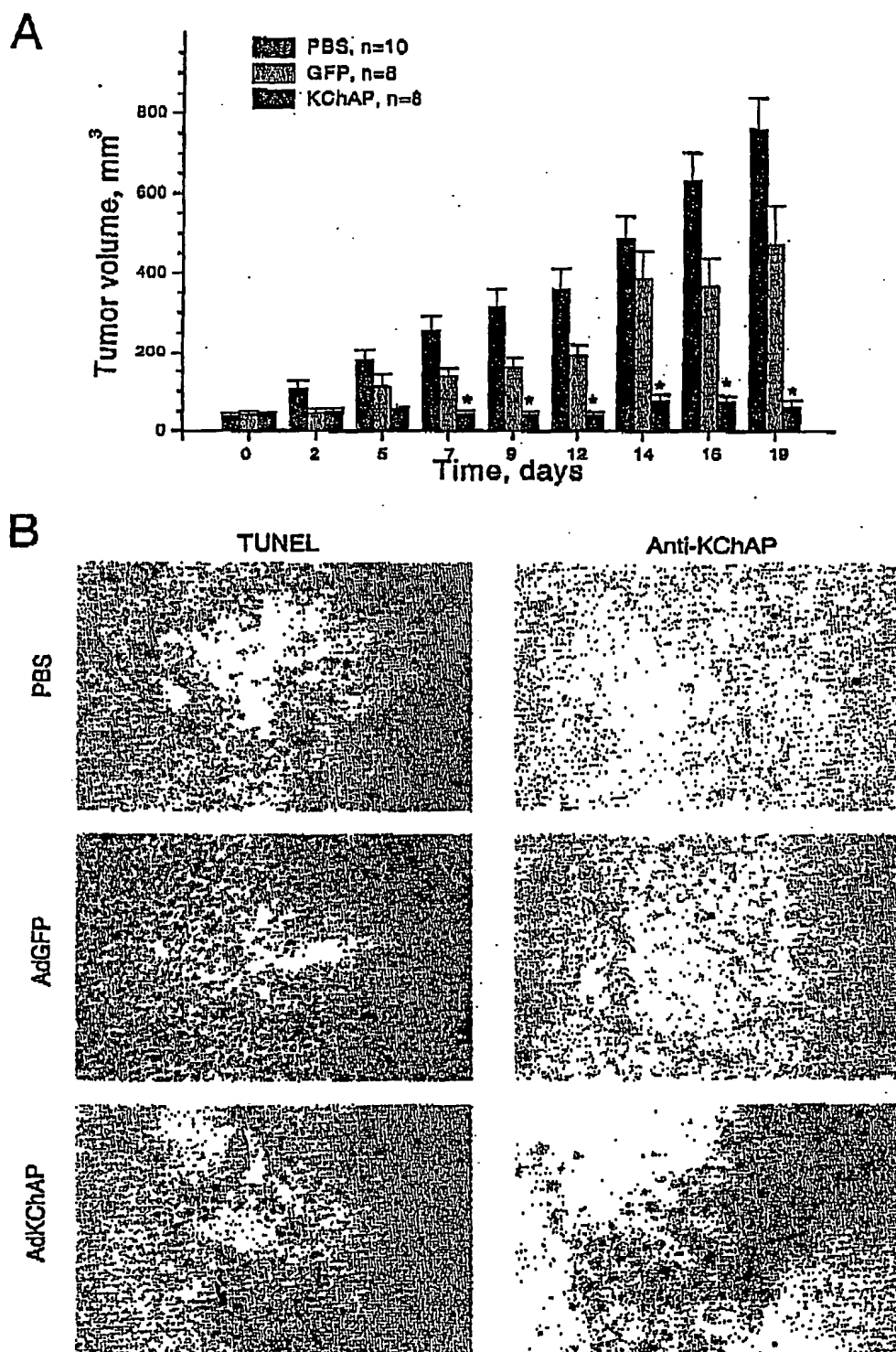


Fig. 9A

A  
P  
a  
I

1 atgaagatcaaagagctttaccgacgacgctttccccggaagaccctggggccctctgat 60  
-----+-----+-----+-----+-----+  
M K I K E L Y R R R F P R K T L G P S D -

61 ctctcccttctctcttttggccctggcaccctctcctgtaggctcccttggtcctctagct 120  
-----+-----+-----+-----+-----+  
L S L L S L P P G T S P V G S P G P L A -

A  
P  
a  
I

121 cccattcccccaacgctgttgccccctggcaccctgctgggcccccaagcgtgaggtggac 180  
-----+-----+-----+-----+-----+  
P I P P T L L A P G T L L G P K R E V D -

181 atgcacccccctctgccccagcctgtgcaccctgatgtcaccatgaaaccattgccttc 240  
-----+-----+-----+-----+-----+  
M H P P L P Q P V H P D V T M K P L P F -

241 tatgaagtctatggggagctcatccggccccaccacccttgcacccacttctagccagcgg 300  
-----+-----+-----+-----+-----+  
Y E V Y G E L I R P T T L A S T S S Q R -

301 tttgaggaagcgcactttacctttgccctcacacccagcaagtgcagcagattcttaca 360  
-----+-----+-----+-----+-----+  
F E E A H F T F A L T P Q Q V Q Q I L T -

361 tccagagaggttctgccaggagccaaatgtgattataccatacaggtgcagctaaagttc 420  
-----+-----+-----+-----+-----+  
S R E V L P G A K C D Y T I Q V Q L R F -

P  
V  
u  
I  
I

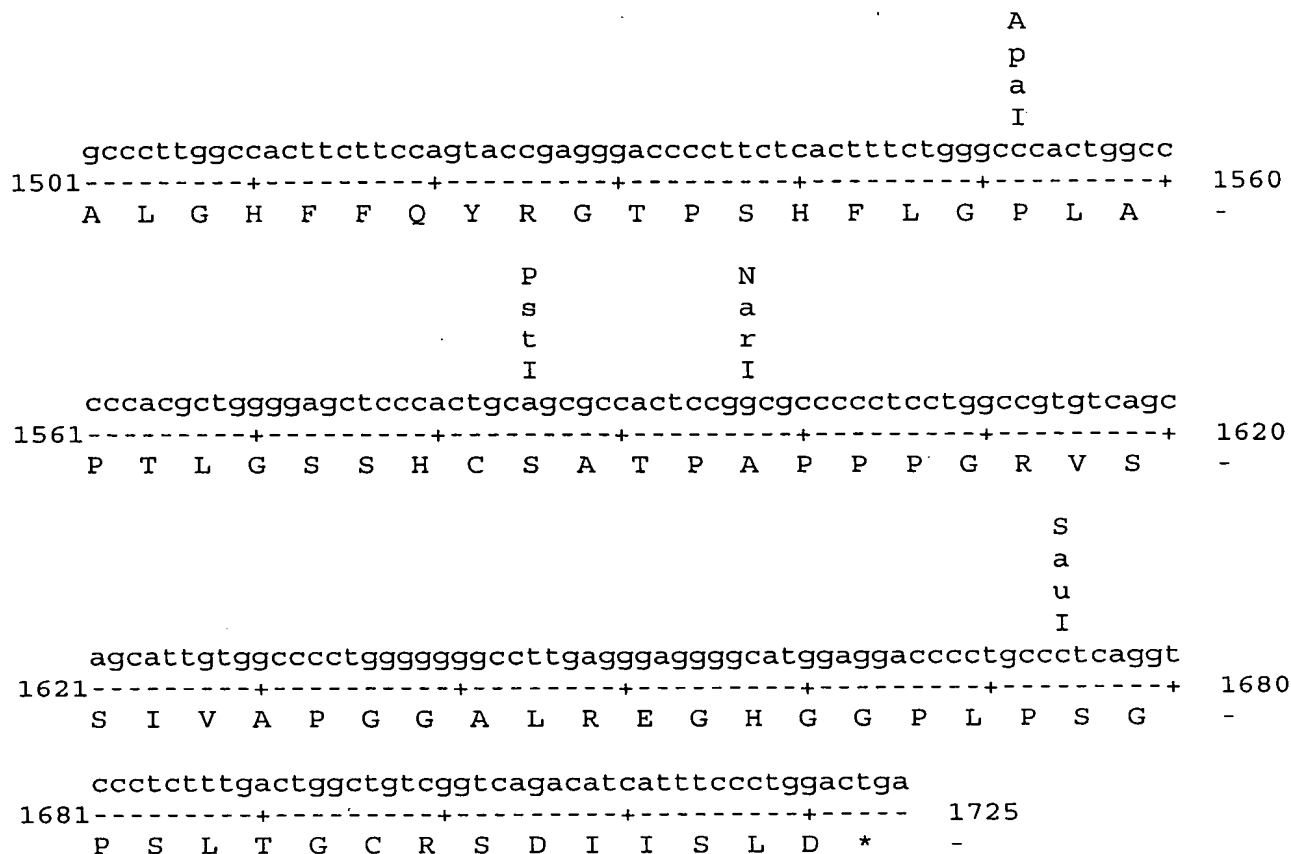
421 tgtctctgtgagaccagctgccccaggaagattattttccccaacctctttgtcaag 480  
-----+-----+-----+-----+-----+  
C L C E T S C P Q E D Y F P P N L F V K -



Fig. 9C

	P	B																			
	f	a																			
	l	m																			
	M	H																			
	I	I																			
1021	gatgagatccaattcatggaagatggatcctggtgcccaatgaaaccaagaaggaggca																1080				
	D	E	I	Q	F	M	E	D	G	S	W	C	P	M	K	P	K	K	E	A	-
									P												
									f												
									l												
									M												
									I												
1081	tctgaggtttgcccccgccagggtatgggctggatggcctccagtacagcccaggtccag																1140				
	S	E	V	C	P	P	P	G	Y	G	L	D	G	L	Q	Y	S	P	V	Q	-
1141	gggggagatccatcagagaataagaagaagggtcgaagtatttgacttgacaatagaaagc																1200				
	G	G	D	P	S	E	N	K	K	K	V	E	V	I	D	L	T	I	E	S	-
																		P			
																		v			
																		u			
																		I			
																		I			
1201	tcatcagatgaggaggatctgccccctaccaagaagcactgttctgtcacctcagctgcc																1260				
	S	S	D	E	E	D	L	P	P	T	K	K	H	C	S	V	T	S	A	A	-
1261	atccccggccctacctggaagcaaaggagtcctgacatctggccaccagccatcctcggtg																1320				
	I	P	A	L	P	G	S	K	G	V	L	T	S	G	H	Q	P	S	S	V	-
1321	ctaaggagccctgctatgggcacgttgggtggggatttcctgtccagtcctccactacat																1380				
	L	R	S	P	A	M	G	T	L	G	G	D	F	L	S	S	L	P	L	H	-
1381	gagtaccacactgccttcccactgggagccgacatccaaggtttagattttattttcattt																1400				
	E	Y	P	P	A	F	P	L	G	A	D	I	Q	G	L	D	L	F	S	F	-
1441	cttcagacagagagtcagcactatggccccctctgtcatcacctcactagatgaacaggat																1500				
	L	Q	T	E	S	Q	H	Y	G	P	S	V	I	T	S	L	D	E	Q	D	-

Fig. 9D



Enzymes that do cut:

ApaI  
SauI

BamHI

BsaWI

BstEII

NarI

PflMI

PstI

PvuII

Enzymes that do not cut:

AatII  
BsmI  
EcoRI  
NotI  
SfiIAgeI  
BssHII  
HindIII  
NruI  
SmaIAseI  
BstBI  
HpaI  
NsiI  
SnaBIAvaI  
BstXI  
KpnI  
PmlI  
SpeIBbrPI  
ClaI  
MluI  
PvuI  
SspIBfrI  
DraI  
NcoI  
SacII  
StuIBglII  
DraIII  
NdeI  
SalI  
XbaIBsaBI  
EagI  
NheI  
ScaI  
XhoI

Fig. 10

hPIAS1	MDGAEKQWYSEL	RVSEIQVLLGYAGRN	KHGRKHELLKRAHL	LKAGCCPAVQMKIKE	LYERFPQIMTPAD	LSIPNVH-----S	82
mPIAS1	.....F	.....S	.....A	.....SS.A.S	.....R.TIG.S	.....L-----LSLPGT	82
mPIAS3	.....F	.....S	.....D	.....S	.....Y.RTLEGLS	.....TIKSSVFSLOGG	75
hPIASx $\alpha$	.....FE.RN.S.F	.....F	.....S	.....D	.....Y.RTLEGLS	.....TIKSSVFSLOGG	89
hPIASx $\beta$	.....FE.RN.S.F	.....F	.....S	.....D	.....Y.RTLEGLS	.....TIKSSVFSLOGG	89
hPIASy	MA.ELV.A.N...F	D.M...FV.S	S.L...V.R.Q	VQFD...ELPK	ET.YAK.NGE.P	-----QPHRPL	81
hPIAS1	SPMPATLSPS---	TI	PQUTYDGHPRASSPLL	PVSLGPRKLELPH	LTSALHFVHDIKQ	KLPTVDLLDELIKPT	169
mPIAS1	.....P	.....E	.....	.....	.....	.....	169
mPIAS3	.....VEPD.AVAGTHSL	STSVTP.SP	VG.S.L.QDT.PTF	MQQ	PSPPIP	.....VQ.K.N	116
hPIASx $\alpha$	.....VEPD.AVAGTHSL	STSVTP.SP	VG.S.L.QDT.PTF	MQQ	PSPPIP	.....VQ.K.N	179
hPIASx $\beta$	D.LTNHSTYDRAGAV	STPLA.FNIDY.V	YGYK.NGIGR	-----	PATLK.EVR.V	.....FIM	164
hPIASy	AFALTRQVQVQI	SSS	MD-1SGTKCDFTVQV	QLRFCLSETSCQED	HPFFNLQVNTKPC	SLPGVLPFKNGVPEP	258
mPIAS1	.....L	.....UT	REVLP.A	Y.I	.....C	.....Y	258
mPIAS3	.....L	.....UT	REVLP.A	Y.I	.....C	.....Y	264
hPIASx $\alpha$	.....RE.CI	R.FLP.GRR.Y	.....L.A	.....NY.NS	I	G.LF.P	269
hPIASx $\beta$	.....RE.CI	R.FLP.GRR.Y	.....L.A	.....NY.NS	I	G.LF.P	269
hPIASy	I	.....R	EL.RKF	QGNQF.V	---A	V.I.Y.D	251
hPIAS1	STTVPTNMG-SWTAE	IGR	---NYSRAVYL	VQLSSTVLLQLEA	KGIENPHSRALIKE	KLTADPDSEIATTS	343
mPIAS1	.....IVV	.....	.....	.....	.....	.....	344
mPIAS3	DS---QPLSFTFELL	HLSLDCITPCPC	R	TAGT	.....K	.....	291
hPIASx $\alpha$	.....SA	QISI	AS	.....K	.....S	VR.T.AM	355
hPIASx $\beta$	.....SA	QISI	AS	.....K	.....S	VR.T.AM	355
hPIASy	SAT-RJTVT.GNY	-K	---S.V.L	VR.T.SE	.....KT	I.VKH.ELCK.V	335
hPIAS1	PCRALTCSTLQCFDA	TLYIQMNEKFTWQ	.....	.....	.....	.....	425
mPIAS1	.....A	.....S	.....A	.....S	.....S	.....S	426
mPIAS3	.....A	.....S	.....A	.....S	.....S	.....S	373
hPIASx $\alpha$	.....V	.....T	.....A	.....S	.....L	.....ND	437
hPIASx $\beta$	.....V	.....T	.....A	.....S	.....L	.....ND	437
hPIASy	.....E	.....A	.....V	.....P	.....DQ	.....LSK	425
hPIAS1	ASYN-GVDCGL---	SSTLEKQVA--SHHQ	SSNKKKKVEVIDUTI	.....	.....	.....	491
mPIAS1	.....N	.....	.....	.....	.....	.....	494
mPIAS3	PPPGY.L	.....QYSAV--QEGI	OPEEK.R	.....	.....	.....	438
hPIASx $\alpha$	SO-----PCTKIES	V.SKPCS--VTVA	EASK	D	.....	.....	503
hPIASx $\beta$	SO-----PCTKIES	VLSKPCS--VTVA	EASK	D	.....	.....	503
hPIASy	P.DAN.LLPAPSVNG	GA.GSTGGGCPVGS	ME.GKPGAD.V	.....L	.....	.....	510
hPIAS1	ILSLPHQASPVSRTP	SLPAVDTSYINTSLI	QDYRHEPH-MTP	---	.....	.....	579
mPIAS1	.....	.....	.....	.....	.....	.....	580
mPIAS3	V.TSGI	P.S.L.S	AMKTLGSDFLS---	---	SL.V.EYP	AFP	515
hPIASx $\alpha$	V.M--Y.P.S--V	VTS	PAA.PP	T	SV	H.1SS	550
hPIASx $\beta$	V.M--Y.P.S--V	VTS	PAA.PP	T	SV	H.1SS	563
hPIAS1	FFVTSKQWFLIQLEA	G-GTSLPTNGSSS	GSNSLSVS-SNSLSE	SHSHVTNRSTDTA	SIFGIIPDISUD*	.....	650
mPIAS1	.....A	.....	.....	.....	.....	.....	651
mPIAS3	QYRGTPSH	GP.AP	TL..CHGSS.PAPPP	RV	I	AKSSS	583
hPIASx $\alpha$	-----EQRENDINH	E-LKLGTSSTVQ*	.....	.....	.....	.....	572
hPIASx $\beta$	CPP	.....S	TS	P-LTA	STSVMTT	.....	621

Fig. 11

KChAP expression in Human Brain Tumors and  
Colon Cancers

	C#64	C#65	
HumI	N	T	N
	46	54	61
	64	71	85
	86		

